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SEQUENCE LISTING



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Abell, Christopher
Inoue, Tsuyoshi
von Delft, Frank

<120> Crystal Structure

<130> 620-139

<140> US 09/820,745
<141> 2001-03-30

<160> 12

<170> PatentIn Ver. 2.1

<210> 1
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved sequence motif

<400> 1
Leu Val Gly Asp Ser Leu Gly Met
1 5

<210> 2
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved sequence motif

<400> 2
Val Lys Ile Glu Gly Gly
1 5

<210> 3
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved sequence motif

<220>
<221> SITE
<222> (3)
<223> Xaa is a hydrophobic residue

<400> 3
Gly His Xaa Gly Leu Thr Pro Gln
1 5

<210> 4
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved sequence motif

<400> 4
Gly Gly Tyr Lys Val Gln Gly
1 5

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved sequence motif

<400> 5
Ile Gly Ile Gly Ala Gly
1 5

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved sequence motif

<400> 6
Asp Gly Asn Ile Leu Val
1 5

<210> 7
<211> 264
<212> PRT
<213> Escherichia coli

<400> 7

```
Met Lys Pro Thr Thr Ile Ser Leu Leu Gln Lys Tyr Lys Gln Asp Lys
  1               5                  10                  15

Lys Arg Phe Ala Thr Ile Thr Ala Tyr Asp Tyr Ser Phe Ala Lys Leu
             20                  25                  30

Phe Ala Asp Glu Gly Leu Asn Val Met Leu Val Gly Asp Ser Leu Gly
         35                  40                  45

Met Thr Val Gln Gly His Asp Ser Thr Leu Pro Val Thr Val Ala Asp
     50                  55                  60

Ile Ala Tyr His Thr Ala Ala Val Arg Arg Gly Ala Pro Asn Cys Leu
 65                  70                  75                  80

Leu Leu Ala Asp Leu Pro Phe Met Ala Tyr Ala Thr Pro Glu Gln Ala
                 85                  90                  95

Phe Glu Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Met Val Lys
            100                 105                 110

Ile Glu Gly Gly Glu Trp Leu Val Glu Thr Val Gln Met Leu Thr Glu
        115                 120                 125

Arg Ala Val Pro Val Cys Gly His Leu Gly Leu Thr Pro Gln Ser Val
    130                 135                 140

Asn Ile Phe Gly Gly Tyr Lys Val Gln Gly Arg Gly Asp Glu Ala Gly
145                 150                 155                 160

Asp Gln Leu Leu Ser Asp Ala Leu Ala Leu Glu Ala Ala Gly Ala Gln
                165                 170                 175

Leu Leu Val Leu Glu Cys Val Pro Val Glu Leu Ala Lys Arg Ile Thr
            180                 185                 190

Glu Ala Leu Ala Ile Pro Val Ile Gly Ile Gly Ala Gly Asn Val Thr
        195                 200                 205

Asp Gly Gln Ile Leu Val Met His Asp Ala Phe Gly Ile Thr Gly Gly
    210                 215                 220

His Ile Pro Lys Phe Ala Lys Asn Phe Leu Ala Glu Thr Gly Asp Ile
225                 230                 235                 240

Arg Ala Ala Val Arg Gln Tyr Met Ala Glu Val Glu Ser Gly Val Tyr
                245                 250                 255

Pro Gly Glu Glu His Ser Phe His
            260
```

<210> 8
<211> 267
<212> PRT
<213> Schizosaccharomyces pombe

<400> 8

```
Met Ser Leu Lys Gln Ile Thr Ile Ser Thr Leu Arg Gln Trp Lys Leu
  1               5                  10                  15

Ala Asn Lys Lys Phe Ala Cys Ile Thr Ala Tyr Asp Ala Ser Phe Ser
             20                  25                  30

Arg Leu Phe Ala Glu Gln Gly Met Pro Val Met Leu Val Gly Asp Ser
         35                  40                  45

Leu Gly Met Thr Ala Gln Gly His Ser Thr Thr Leu Pro Val Ser Val
     50                  55                  60

Glu Asp Ile Ala Tyr His Thr Lys Ser Val Arg Arg Gly Ala Pro Asn
 65                  70                  75                  80

Arg Leu Leu Met Ala Asp Leu Pro Phe Met Ser Tyr Ser Thr Trp Glu
                 85                  90                  95

Asp Ala Cys Lys Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Ile
            100                 105                 110

Val Lys Ile Glu Gly Gly Gly Asn Trp Ile Phe Glu Ile Val Gln Arg
        115                 120                 125

Leu Thr Glu Arg Ser Val Pro Val Ala Gly His Leu Gly Leu Thr Pro
    130                 135                 140

Gln Ser Val Asn Ile Phe Gly Gly Tyr Lys Ile Gln Gly Arg Glu Gln
145                 150                 155                 160

Ser Ala Ala Ala Arg Leu Ile Glu Asn Ala Gln Gln Leu Glu Lys Phe
                165                 170                 175

Gly Ala Gln Leu Leu Val Leu Glu Cys Ile Pro Glu Ser Leu Ala Glu
            180                 185                 190

Gln Ile Thr Lys Thr Ile Ser Ile Pro Thr Ile Gly Ile Gly Ala Gly
        195                 200                 205

Lys His Thr Asp Gly Gln Ile Leu Val Met His Asp Ala Leu Gly Ile
    210                 215                 220

Thr Gly Gly Arg Pro Pro Lys Phe Ala Lys Asn Phe Leu Ser Gly Ala
225                 230                 235                 240

Gly Asp Ile Arg Thr Ala Ile Gln Arg Tyr Ile Tyr Glu Val Glu Gln
                245                 250                 255

Gly Leu Tyr Pro Ala Glu Glu His Ser Phe Gln
            260                 265
```

<210> 9
<211> 349
<212> PRT
<213> Aspergillus nidulans

<400> 9

```
Met Thr Phe Leu Arg Ile Ala Thr Lys Arg Ala Ile Tyr Leu His Arg
  1               5                  10                  15

Pro Ala Asn Pro Ala Leu Pro Thr Ser Ser Ile Leu Pro Val Leu His
            20                  25                  30

Ser Thr Asn Val Ala Thr Arg Val Pro Ser Pro Cys Ala Ile Arg His
        35                  40                  45

Ser Ser His Ser Pro Leu Gly Ala Ala Gln Ala Asn Pro Arg Lys Lys
    50                  55                  60

Val Thr Met Gln Thr Leu Arg Asn Leu Tyr Lys Lys Gly Glu Pro Ile
65                  70                  75                  80

Thr Met Leu Thr Ala His Asp Phe Pro Ser Ala His Val Ala Asp Ala
                85                  90                  95

Ala Gly Met Asp Met Ile Leu Val Gly Asp Ser Leu Ala Met Val Ala
            100                 105                 110

Leu Gly Met Gln Asp Thr Ser Glu Val Thr Leu Asp Asp Met Leu Val
        115                 120                 125

His Cys Arg Ser Val Ala Arg Ala Ala Gln Ser Ala Phe Thr Val Ser
    130                 135                 140

Asp Leu Pro Met Gly Ser Tyr Glu Val Ser Pro Glu Gln Ala Leu Gln
145                 150                 155                 160

Ser Ala Ile Arg Ile Val Lys Glu Gly Arg Val Gln Gly Val Lys Leu
                165                 170                 175

Glu Gly Gly Glu Glu Met Ala Pro Ala Ile Lys Arg Ile Thr Thr Ala
            180                 185                 190

Gly Ile Pro Val Val Gly His Ile Gly Leu Thr Pro Gln Arg Gln Asn
        195                 200                 205

Ala Leu Gly Gly Phe Arg Val Gln Gly Lys Ser Thr Thr Asp Ala Leu
    210                 215                 220

Lys Leu Leu Lys Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Met
225                 230                 235                 240

Ile Val Ile Glu Ala Val Pro Pro Glu Ile Ala Ser Ile Val Thr Gln
                245                 250                 255

Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Cys Ser
            260                 265                 270
```

```
Gly Gln Val Leu Val Gln Ile Asp Met Thr Gly Asn Phe Pro Pro Gly
        275                 280                 285

Arg Phe Leu Pro Lys Phe Val Lys Gln Tyr Ala Asn Val Trp Asn Glu
    290                 295                 300

Ala Leu Gln Gly Ile Gln Gln Tyr Arg Glu Glu Val Lys Ser Arg Ala
305                 310                 315                 320

Tyr Pro Ala Glu Gln His Thr Tyr Pro Ile Pro Lys Glu Glu Leu Val
                325                 330                 335

Glu Phe Gln Lys Ala Val Asp Glu Leu Pro Glu Glu Lys
            340                 345
```

<210> 10
<211> 347
<212> PRT
<213> Arabidopsis thaliana

<400> 10

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Met Ala Ser Ser Leu Thr Arg Asn Cys Ser Arg Phe Ser Lys Ala Ile
  1               5                  10                  15

Ser Val Arg Phe Met Ser Asn Leu Pro Glu Asn Thr Val Tyr Gly Gly
             20                  25                  30

Pro Lys Pro Gln Asn Pro Asn Gln Arg Val Thr Leu Thr His Leu Arg
         35                  40                  45

Gln Lys His Arg Arg Gly Glu Pro Ile Thr Val Val Thr Ala Tyr Asp
     50                  55                  60

Tyr Pro Ser Ala Val His Leu Asp Thr Ala Gly Ile Asp Val Cys Leu
 65                  70                  75                  80

Val Gly Asp Ser Ala Ser Met Val Val His Gly His Asp Thr Thr Leu
                 85                  90                  95

Pro Ile Ser Leu Asp Glu Met Leu Val His Cys Arg Ala Val Ala Arg
            100                 105                 110

Gly Ala Lys Arg Pro Leu Leu Val Gly Asp Leu Pro Phe Gly Thr Tyr
        115                 120                 125

Glu Ser Ser Ser Ser Gln Ala Val Asp Thr Ala Val Arg Val Leu Lys
    130                 135                 140

Glu Gly Gly Met Asp Ala Ile Lys Leu Glu Gly Gly Ser Ala Ser Arg
145                 150                 155                 160

Ile Thr Ala Ala Lys Ala Ile Val Glu Ala Gly Ile Ala Val Ile Gly
                165                 170                 175

His Val Gly Leu Thr Pro Gln Ala Ile Ser Val Leu Gly Gly Phe Arg
            180                 185                 190
```

```
Pro Gln Gly Arg Asn Ile Ala Ser Ala Val Lys Val Val Glu Thr Ala
        195                 200                 205

Met Ala Leu Gln Glu Ala Gly Cys Phe Ser Val Val Leu Glu Cys Val
    210                 215                 220

Pro Pro Pro Val Ala Ala Ala Ala Thr Ser Ala Leu Lys Ile Pro Thr
225                 230                 235                 240

Ile Gly Ile Gly Ala Gly Pro Phe Cys Ser Gly Gln Val Leu Val Tyr
                245                 250                 255

His Asp Leu Leu Gly Met Met Gln His Pro His His Ala Lys Val Thr
            260                 265                 270

Pro Lys Phe Cys Lys Gln Tyr Ala Asn Val Gly Glu Val Ile Asn Lys
        275                 280                 285

Ala Leu Met Glu Tyr Lys Glu Glu Val Ser Lys Lys Val Phe Pro Gly
    290                 295                 300

Pro Ser His Ser Pro Tyr Lys Ile Thr Ala Ser Glu Leu Asp Gly Phe
305                 310                 315                 320

Leu Thr Glu Leu Gln Lys Leu Gly Phe Asp Lys Ala Ala Ser Ala Ala
                325                 330                 335

Ala Leu Ala Ala Glu Asn Met Glu Pro Ser Lys
            340                 345
```

<210> 11
<211> 312
<212> PRT
<213> Saccharomyces cerevisiae

<400> 11

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Met Asn Ile Met Lys Arg Gln Leu Cys Thr Ser Ser Lys Arg Phe Phe
  1               5                  10                  15

Ser Thr Ala Lys Asn Val Val Lys Tyr Asn Thr Ile Gln Asp Ile Arg
             20                  25                  30

Asn Lys Tyr Phe Thr Gly Thr Pro Leu Ser Met Cys Thr Ala Tyr Asp
         35                  40                  45

Phe Ile Thr Ala Thr Trp Val Asn Lys Ala Asn Cys Asp Leu Leu Leu
     50                  55                  60

Val Gly Asp Ser Leu Ala Met Thr Ser Leu Gly Tyr Asp Ser Thr Ile
 65                  70                  75                  80

Thr Leu Ser Leu Asn Glu Phe Lys Tyr His Val Ala Ser Val Cys Arg
                 85                  90                  95

Ala Glu Gly Ser Ser Met Val Val Val Asp Met Pro Phe Gly Thr Phe
            100                 105                 110
```

```
Glu Ser Gly Ile Ser Asp Gly Leu Lys Asn Ala Ile Asp Ile Met Lys
        115                 120                 125

Leu Asp Ser Lys Val Thr Ser Val Lys Val Glu Val Gly Ser Tyr Thr
    130                 135                 140

Lys Asp Lys Tyr Ala Met Lys Phe Ile Glu Glu Leu Cys Ser Arg Gly
145                 150                 155                 160

Ile Pro Val Met Ala His Ile Gly Leu Thr Pro Gln Lys Val His Ser
                165                 170                 175

Leu Gly Gly Tyr Lys Val Gln Gly Ser Lys Ser Leu Leu Gln Met Gln
            180                 185                 190

Glu Leu Tyr Glu Thr Ala Met Gln Leu Gln Lys Ile Gly Cys Trp Ser
        195                 200                 205

Ile Leu Ile Glu Cys Val Pro His Lys Met Ala Gln Phe Ile Thr Ser
    210                 215                 220

Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Thr Ser
225                 230                 235                 240

Gly Gln Val Leu Val Ile Ser Asp Leu Leu Gly Met Gln Gly Asp Ser
                245                 250                 255

Val Pro Lys Phe Val Lys Gln Ala Val Asn Met Thr Asp Ile Ala Thr
            260                 265                 270

Gln Gly Leu Lys Glu Tyr Ile Ala Ser Val Glu Asp Arg Thr Phe Pro
        275                 280                 285

Glu Arg Gly Thr His Thr Phe Lys Val Lys Glu Asp Leu Trp Asn Glu
    290                 295                 300

Phe Leu Ser Ser Ile Asn Glu Lys
305                 310
```

<210> 12
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus

<220>
<221> SITE
<222> 1..4, 6..8, 10..22, 27..29, 31..39, 41, 50..52, 54..56
<223> Xaa is uncertain

<220>
<221> SITE
<222> 59, 62..64, 66, 67, 69..71, 73, 76..81, 83, 88, 89
<223> Xaa is uncertain

<220>
<221> SITE
<222> 91..96, 97..100, 102, 103, 105..108, 110..113, 120..133
<223> Xaa is uncertain

<220>
<221> SITE
<222> 135..138, 140, 142, 145, 151..155, 163, 165..171
<223> Xaa is uncertain

<220>
<221> SITE
<222> 173..175, 177, 179..181, 185, 186, 191, 194, 195
<223> Xaa is uncertain

<220>
<221> SITE
<222> 198..200, 202..205, 208, 215..217, 224, 225, 227, 228
<223> Xaa is uncertain

<220>
<221> SITE
<222> 230..242, 246, 248..258, 260..262, 264..266, 268..271
<223> Xaa is uncertain

<220>
<221> SITE
<222> 274..277, 279..281
<223> Xaa is uncertain

<400> 12

```
Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
  1               5                  10                  15

Xaa Xaa Xaa Xaa Xaa Xaa Thr Ala Tyr Asp Xaa Xaa Xaa Ala Xaa Xaa
             20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Val Gly Asp Ser Leu Gly
         35                  40                  45

Met Xaa Xaa Xaa Gly Xaa Xaa Xaa Thr Leu Xaa Val Thr Xaa Xaa Xaa
     50                  55                  60

Ile Xaa Xaa His Xaa Xaa Xaa Val Xaa Arg Gly Xaa Xaa Xaa Xaa Xaa
 65                  70                  75                  80

Xaa Leu Xaa Asp Leu Pro Phe Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95

Ala Xaa Xaa Xaa Ala Xaa Xaa Val Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa
            100                 105                 110

Xaa Val Lys Ile Glu Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115                 120                 125

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Val Xaa Val Xaa Gly His
    130                 135                 140
```

Xaa Gly Leu Thr Pro Gln Xaa Xaa Xaa Xaa Xaa Gly Gly Tyr Lys Val
145 150 155 160

Gln Gly Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Ala
165 170 175

Xaa Ala Xaa Xaa Xaa Ala Gly Ala Xaa Xaa Leu Val Leu Glu Xaa Val
180 185 190

Pro Xaa Xaa Leu Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Ile Pro Xaa
195 200 205

Ile Gly Ile Gly Ala Gly Xaa Xaa Xaa Asp Gly Gln Ile Leu Val Xaa
210 215 220

Xaa Asp Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225 230 235 240

Xaa Xaa Pro Lys Phe Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
245 250 255

Xaa Xaa Ala Xaa Xaa Xaa Tyr Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Tyr
260 265 270

Pro Xaa Xaa Xaa Xaa His Xaa Xaa Xaa
275 280